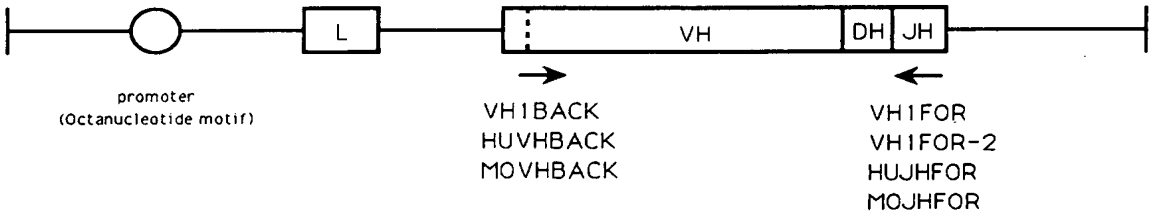
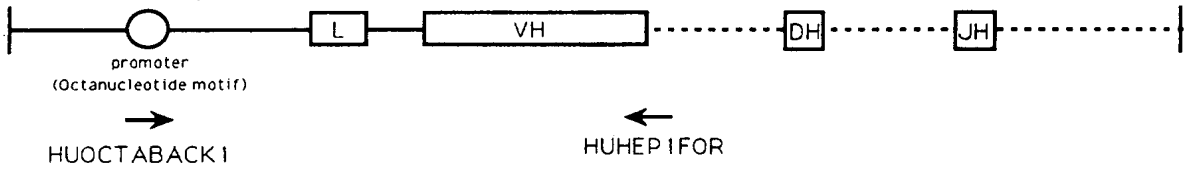
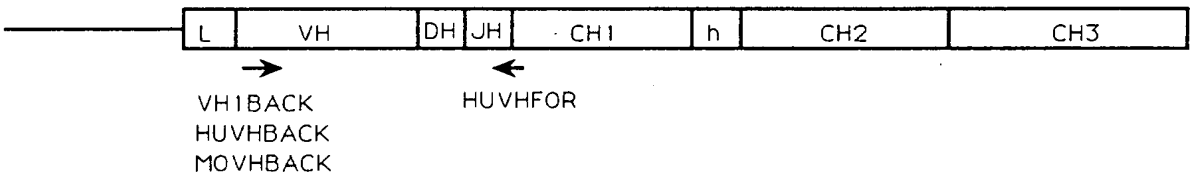
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

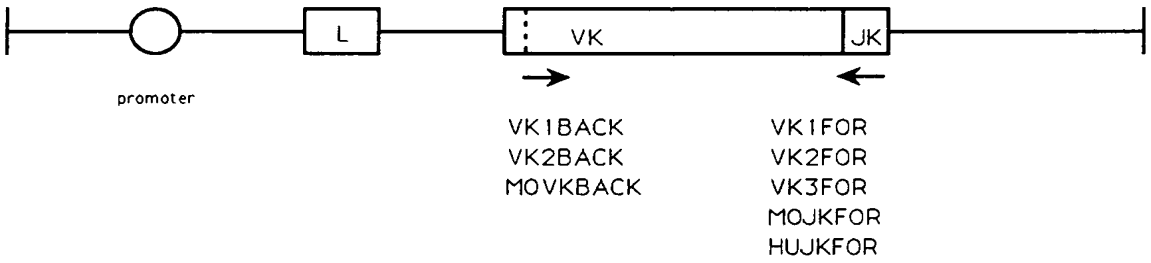


FIG. 1

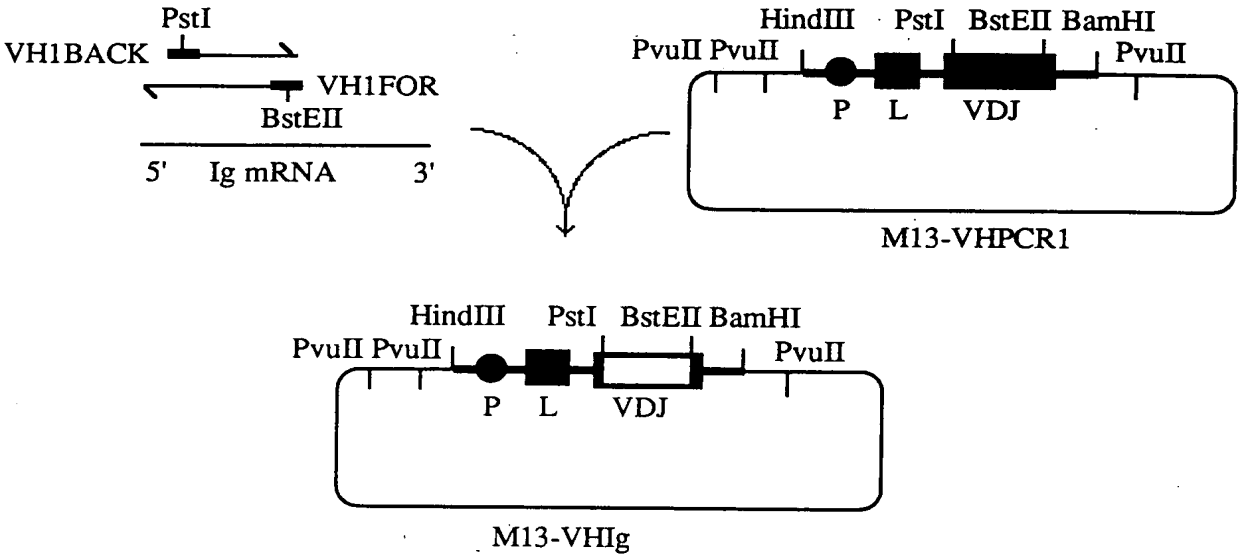


FIG. 2

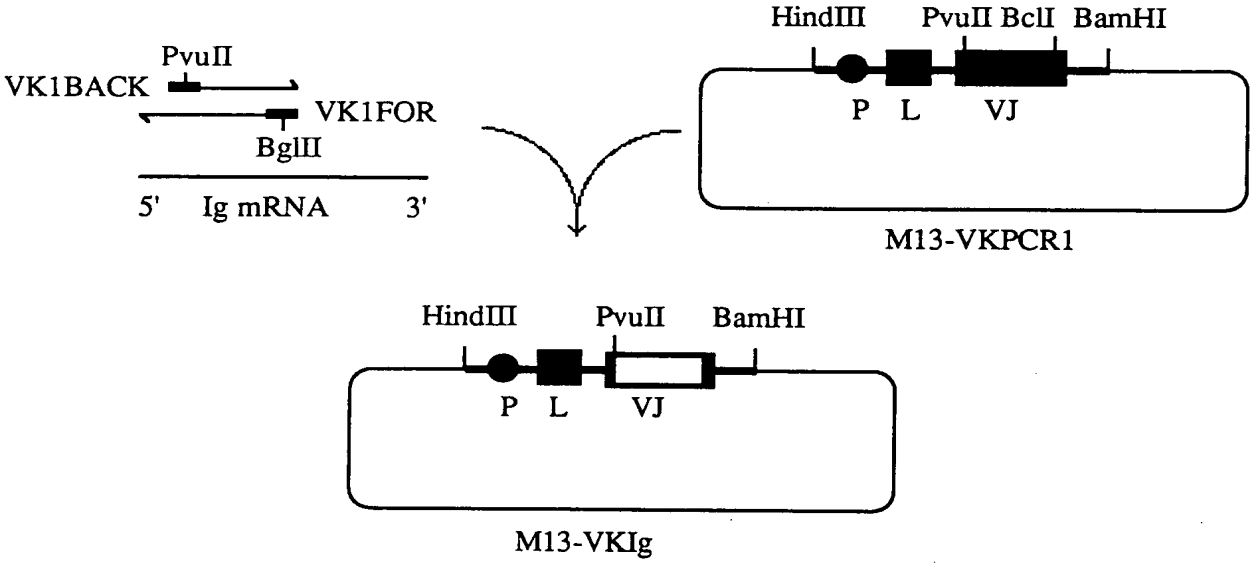


FIG. 4

M13 VHPCR1.

HinD III (1)

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTTGTCTATACCA
10 20 30 40 50 60

CAAACAGAAAAACATGAGATCACAGTTCTCTCTACAGTTACTGAGCACACAGGACCTCAC
70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
130 140 150 160 170 180

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAATGACATCCACTTTGCCTTTC
190 200 210 220 230 240

PstI
1 5 10
G V H S Q V Q L Q E S G P G L V R P
TCTCCACAGGTGTCCACTCCCAGGTCCAACTGCAGGAGAGCGGTCCAGGTCTTGTGAGAC
250 260 270 280 290 300

CDR1
15 20 25 30
S Q T L S L T C T V S G S T F S S Y W M
CTAGCCAGACCCTGAGCCTGACCTGCACCGTGTCTGGCAGCACCTTCAGCAGCTACTGGA
310 320 330 340 350 360

CDR2
35 40 45 50
H W V R Q P P G R G L E W I G R I D P N
TGCACTGGGTGAGACAGCCACCTGGACGAGGTCTTGAGTGGATTGGAAGGATTGATCCTA
370 380 390 400 410 420

55 60 65 70
S G G T K Y N E K F K S R V T M L V D T
ATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAGAGTGACAATGCTGGTAGACA
430 440 450 460 470 480

75 80 85 90
S K N Q F S L R L S S V T A A D T A V Y
CCAGCAAGAACCAGTTCAGCCTGAGACTCAGCAGCGTGACAGCCGCCGACACCGCGGTCT
490 500 510 520 530 540

CDR3
95 100 105 110
Y C A R Y D Y Y G S S Y F D Y W G Q G T
ATTATTGTGCAAGATACGATTACTACGGTAGTAGCTACTTTGACTACTGGGGCCAAGGGA
550 560 570 580 590 600

BstEII
115 120
T V T V S S
CCACGGTCACCGTCTCCTCAGGTGAGTCCTTACAACCTCTCTCTTCTATTCAGCTTAAAT
610 620 630 640 650 660

AGATTTTACTGCATTTGTTGGGGGGGAAATGTGTGTATCTGAATTTCAGGTCATGAAGGA
670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGGTCATTGGGAGCCCGGGCTGATGCAGACAGACA
730 740 750 760 770 780

BamHI
TCCTCAGCTCCCAGACTTCATGGCCAGAGATTTATAG
790 800 810

FIG. 3

M13 VkPCR1

HinD III

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTTGTCTATACCA
38 48 58 68 78 88

CAAACAGAAAAACATGAGATCACAGTTCTCTCTACAGTTACTGAGCACACAGGACCTCAC
98 108 118 128 138 148

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
158 168 178 188 198 208

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAATGACATCCACTTTGCCTTTC
218 228 238 248 258 268

Pvu II

1 5 10
G V H S D I Q L T Q S P S S L S A S
TCTCCACAGGTGTCCACTCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCA
278 288 298 308 318 328

CDR1

15 20 25 30
V G D R V T I T C *R A S G N I H N Y L A*
GCGTGGGTGACAGAGTGACCATCACCTGTAGAGCCAGCGGTAACATCCACAACTACCTGG
338 348 358 368 378 388

CDR2

35 40 45 50
W Y Q Q K P G K A P K L L I Y *Y T T T L*
CTTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACTACACCACCACCC
398 408 418 428 438 448

55 60 65 70
A D G V P S R F S G S G S G T D F T F T
TGGCTGACGGTGTGCCAAGCAGATTCAGCGGTAGCGGTAGCGGTACCGACTTCACCTTCA
458 468 478 488 498 508

CDR3

75 80 85 90
I S S L Q P E D I A T Y Y C *Q H F W S T*
CCATCAGCAGCCTCCAGCCAGAGGACATCGCCACCTACTACTGCCAGCACTTCTGGAGCA
518 528 538 548 558 568

Bcl I (requires *dam*⁻ host)

95 100 105 108
P R T F G Q G T K V V I K R
CCCCAAGGACGTTCGGCCAAGGGACCAAGGTGGTGATCAAACGTGAGTAGAATTTAAACT
578 588 598 608 618 628

BamHI

TTGCTTCCTCAGTTGGATCC
638 648

FIG. 5

Sequence of MBr1 VH

```
                                                                  Splice      -1
                                                                    ↓G  V  H  S
                                                                  AGGTGTCCACTCC
 1          PstI                  10                                       20
 Q  V  Q  L  Q  E  S  G  T  E  L  A  S  P  G  A  S  V  T  L
CAGGTCCAACTGCAGGAGTCAGGAACTGAGCTGGCGAGTCCTGGGGCATCAGTGACACTG
  VH1BACK SITE
                                30      CDR1                              40
 S  C  K  A  S  G  Y  T  F  T  D  H  I  I  N  W  V  K  K  R
TCCTGCAAGGCTTCTGGCTACACATTTACTGACCATATTATAAATTGGGTAAAAAAGAGG
                                              52a 53     CDR2
 P  G  Q  G  L  E  W  I  G  R  I  Y  P  V  S  G  V  T  N  Y
CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTTATCCAGTAAGTGGTGTAACTAACTAC
60   CDR2      65                70
 N  Q  K  F  M  G  K  A  T  F  S  V  D  R  S  S  N  T  V  Y
AATCAAAAATTCATGGGCAAGGCCACATTCTCTGTAGACCGGTCCTCCAACACAGTGTAC
80       82A  B  C 83                        90                CDR3
 M  V  L  N  S  L  T  S  E  D  P  A  V  Y  Y  C  G  R  G  F
ATGGTGTTGAACAGTCTGACATCTGAGGACCCTGCTGTCTATTACTGTGGAAGGGGCTTT
   CDR3    103                BstEII          Splice
 D  F  D  Y  W  G  Q  G  T  T  V  T  V  S  S  ↓
GATTTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGT.....
                    VH1FOR SITE
```

Sequence of MBr1 VK

```
                                                                  Splice      -1
                                                                    ↓G  V  H  S
                                                                  AGGTGTCCACTCC
 1     PvuII                 10                                       20
 D  I  Q  L  T  Q  S  P  P  S  L  T  V  S  V  G  E  R  V  T
GACATTCAGCTGACCCAGTCTCCACCATCCCTGACTGTGTCAGTAGGAGAGAGGGTCACT
    VK1BACK SITE
                        27A  B  C  D  E  F     CDR1
 I  S  C  K  S  N  Q  N  L  L  W  S  G  N  R  R  Y  C  L  G
ATCAGTTGCAAATCCAATCAGAATCTTTTATGGAGTGGAAACCGAAGGTACTGTTTGGGC
35              40                                    50    CDR2
 W  H  Q  W  K  P  G  Q  T  P  T  P  L  I  T  W  T  S  D  R
TGGCACCAGTGGAAACCAGGGCAAACTCCTACACCGTTGATCACCTGGACATCTGATAGG
                60                                    70
 F  S  G  V  P  D  R  F  I  G  S  G  S  V  T  D  F  T  L  T
TTCTCTGGAGTCCCTGATCGTTTCATAGGCAGTGGATCTGTGACAGATTTCACTCTGACC
                80                                    90    CDR3
 I  S  S  V  Q  A  E  D  V  A  V  Y  F  C  Q  Q  H  L  D  L
ATCAGCAGTGTGCAGGCTGAAGATGTGGCAGTTTATTTCTGTCAGCAACATTTGGACCTT
95              100           BglII/BclI Splice
 P  Y  T  F  G  G  G  T  K  L  E  I  K  ↓
CCGTACACGTTCGGAGGGGGGACCAAGCTGGAGATCAAACGTGAG
                  VK1FOR SITE
```

FIG. 6

α-Lys 30

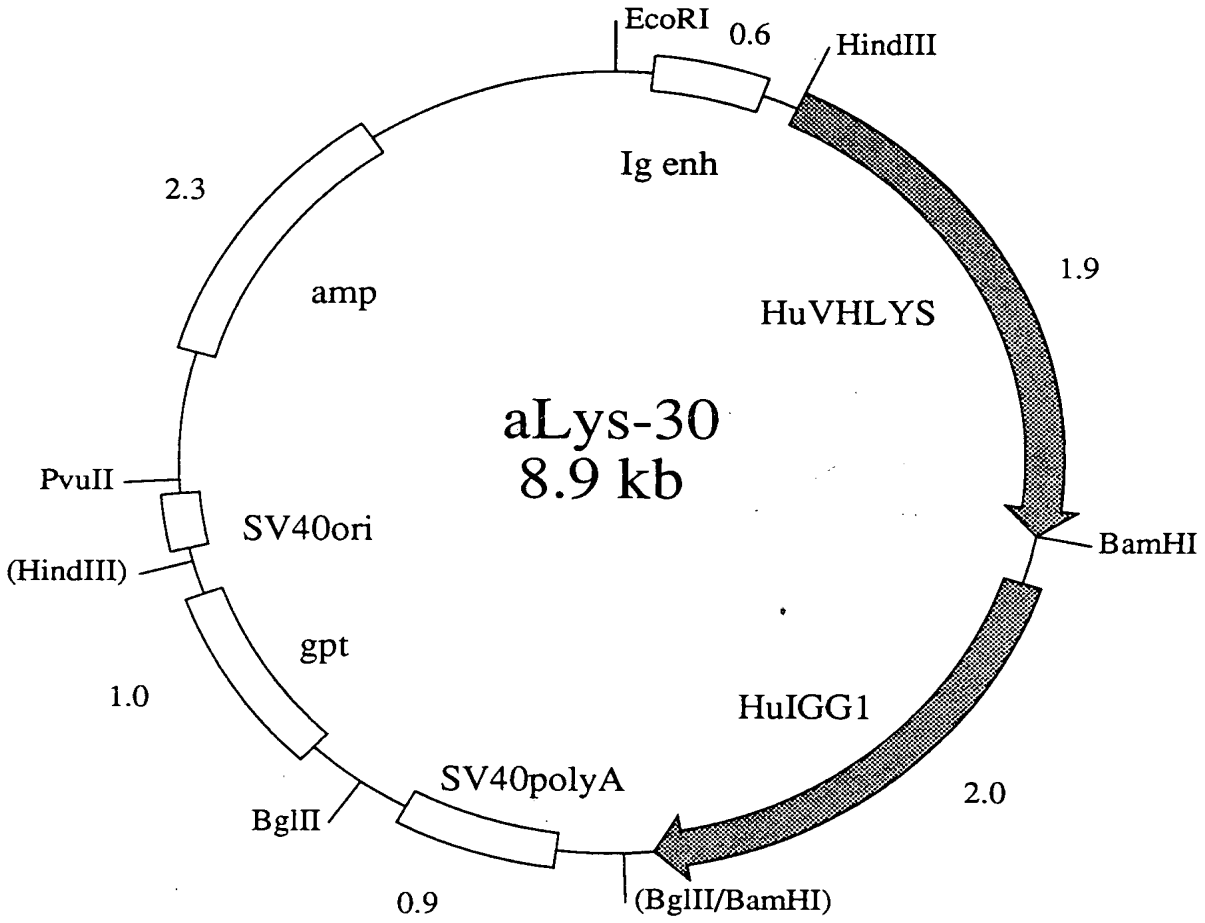


FIG. 7

α-Lys 17

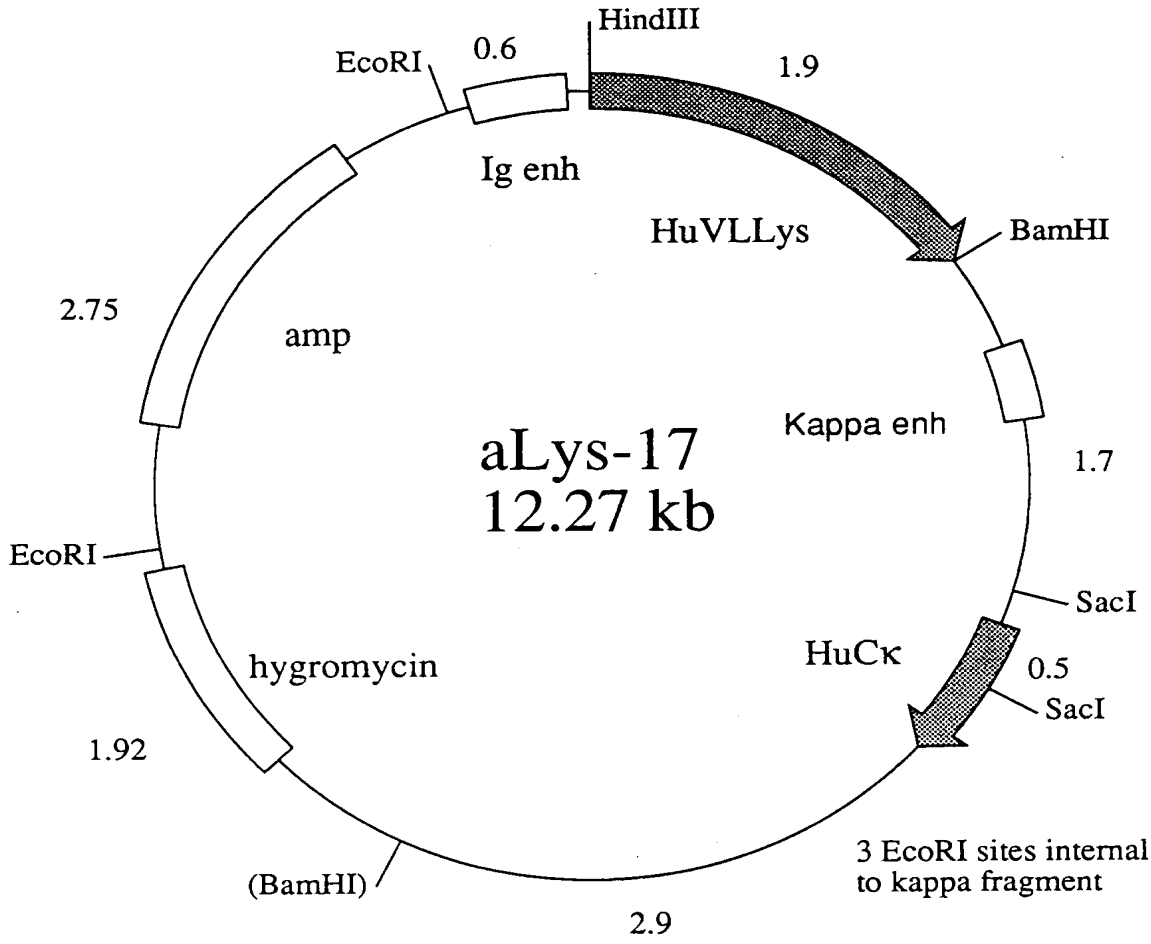


FIG. 8

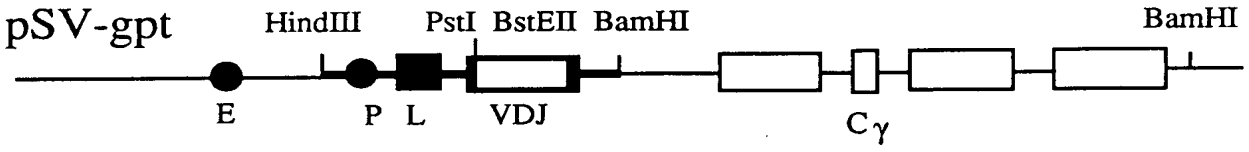
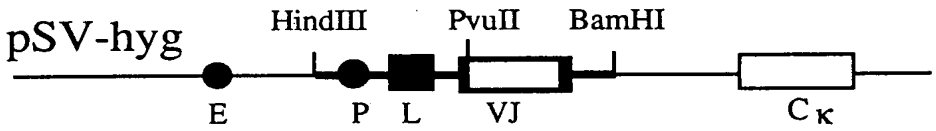


FIG. 9



	FR1	CDR 1	FR2	CDR 2
KABAT IA				
A07	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
A09	PGLVKPSQSLFLTCSITGFPIT	SGYYWI	WIRQSPGKPLEWMG	YITHSGETFYNPSLQS
E03	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
G01	PGLVKPSQSLSLTCSVTGYSIT	SGYYWN	WIRQFPGNKLEWMG	YISYDGSNNYNPSLKN
KABAT IB				
A06	PVLVAPSQSLSITCAVSDFSLT	NYGVL	WVRQPPGKGLEWLG	VIWAGGITNYNSALMS
25G07	PGLVQPSQSLSITCTVSGFSLT	SYGVH	WVRQSPGKGLEWLG	VIWSGGSTDYNAAFIS
B03	PGLVAPSQSLSITCTVSGFSLT	SYGVD	WVRQPPGKGLEWLG	VIWGGGSTNYNSALMS
G03	PGLVQPSQSLSITCTVSGFSLT	SYGVH	WVRQSPGKGLEWLG	VIWSGGSTDYNAAFIS
H09	PVLVAPPQSLSITCTVSGFSLT	SYGVH	WVRQPPGKGLEWLG	VIWAGGSTNYNSALMS
25C10	PGLVAPSQSLSITCTVSGFSLT	SYAIS	WVRQPPGKGLEWLG	VIWTGGGTNYNSALKS
A12	PGLVAPSQSLSITCTVSGFSLT	SYAIS	WVRQPPGKGLEWLG	VIWTGGGTNYNSALKS
A08	PGLVAPSQSLSITCTVSGFSLT	SYGVH	WVRQPPGKGLEW**	*****GSTTYNSALKS
25G08	PGLVAPSQSLSITCTVSGFSLT	SYDVD	WVRQSPGKGLEWLG	VIWGGGSTNYNSALKS
A03	PGLVQPSQSLSITCTVSGFSLT	SYGVH	WVRQSPGKGLEWLG	VIWSGGSTDYNAAFIS
C07	PVLVAPSQSLSITCTVSGFSLT	SYGVH	WVRQPPGKGLEWLG	VIWAGGSTNYNSALMS
H04	PGLVAPSQSLSITCTVSGFSLT	SYGVD	WVRQSPGKGLEWLG	VIWGVGSTNYNSALKS
KABAT IIA				
E04	PELVRPGVSVKISCKGSGYTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQKFKD
H07	PELVRPGVSVKISCKGSGYTFT	DYAMH	WVKQSHAKSLEWIG	VISTYYGDASYNQKFKD
KABAT IIB				
A02	AELVMPGASVKLSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	EIDPSDSYTNYNQKFKG
B04	AELVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPGQGLEWIG	DIYPGSGSTNYNEKFKS
C05	AELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPGRGLEWIG	RIDPNSGGTKYNEKFKS
C09	AELVKPGASLKLSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	EINPSNGGTNYDEKFKS
D06	ASLVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPGQGLEWIG	DIYPGSGSTNYNEKFKS
D08	PELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	EINPSNGGTNYNEKFKS
E07	AELVRPGASVKLSCKASGYTFT	DYEMH	WVKQTPVHGLEWIG	AIDPETGGTAYNQKFKG
G08	PELVKPGASVKISCKASGYTFT	DYYIN	WVKQRPGQGLEWIG	WIYPGSGNTKYNEKFKG
G10	AELVKPGASVKVSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	RIHPSDSDTNYNQKFKG
25G09	AELVKPGASVKMSCKASGYTFT	TYPIE	WVKQNHGKSLEWIG	NFHPYNDDTKYNEKFKG
F04	TELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	NINPSNGGTNYNQKFKG
H02	AELVKPGASVKLSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	NIDPSDSETHYNQKFKD
H01	AELVMPGASVKLSCKASGYTFT	SYWMH	WVKQRPGQGLEWIG	EIDPSDSYTNYN*KVQG
25C05	PELVRPGTSVKMSCKASGYTFF	NYWMK	WV*QRPGQGLEWIG	QIFPASGSIYYNEMHKD
B01	AELVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPGQGLEWIG	DIYPGSGSTNYNEKFKS
B05	AELVRPGSSVKLSCKDSYFAFM	RHAMH	WVKQRPGHGLEWIG	SFTMYSDATEYSENFKG
B11	AELVKPGASVKMSCKASGYTFT	SYWIT	WVKQRPGQGLEWIG	DIYPGSGSTNYNEKFKS
KABAT III A				
25G05	GGLVQAWGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLG	FIRNKANGYTTEYSASVKG
C10	GGLVQPGGSLSLSCAASGFTFT	DYYMN	WVRQPPGKALEWLA	LIRHKANGYTMEYSASVKG
B07	GGLVQPGGSLSLSCAASGFTFT	DYYMS	WVRQPPGKALEWLA	LIRNKANGYTTEYSASVKG
KABAT III B				
G05	GGLVKPGGSLKLSCAASGFTFS	DYGMH	WVRQAPEKGLEWVA	YISSGSSTIYYADTVKG
B12	GGLVQPGESLKLSCESNEYEFP	SHDMS	WVR*********VA	AINSDGGSTYYPDTMER
D04	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISGSGGSTYYADSVKG
D05	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISGSGGSTYYADSVKG
F12	GGLVQPGESWKLSCVIQQ****	*****	WVRQ*PEKRLELVA	AINSDGGSTYYPDTMER
F06	GGLVQPGGSLRLSCAASGFTFS	SYAMS	WVA*APGKGLEWVS	AISGSGGSTYYADSAKG
D02	GGLVQPGESLKLSCESNEYVIP	*HDMS	WVRQDSGE*LELVA	AINSDGGSTYYPDTMER
F09	GDLVKPGGSLKLSCAASGFTFS	SYGMS	WVRQTPDKRLEWVA	TISSGGSYTYYPDSVKG
KABAT III C				
E06	GGLVQPGGSMKLSCAASGFTFS	DAWMD	WVRQSPEKGLEWVA	EIRNKANNHATYYAESVKG
KABAT V A				
C04	AELVKPGASVKLSCKASGYTFT	EYTIH	WVKQRSGQGLEWIG	WFYPGSGSIKYNEKFKD

FIG. 10a

FR 3	CDR 3	
RISITRDTSKNQFFLKLNSVTTEDTATYYCAR	EGNWDGFAY	
PISITRETSKNQFFLQLNSVTTEDTAMYYCAG	DRDKLGPWFAY	
RISITRDTSKNQFFLQLNSVTTEDTATYYCAR	DSSGSMDY	
RISITRDTSKNQFFLKLNSVTTEDTATYYCAR	VSSGYESMDY	
RLSISKDTSKSQVFLKMNSLQTDDTAVYYCAK	HGDSSGYFDY	
RLSISKDNSKSQVFFKMNSLQADDTAIYYCAR	NDGYY	
RLSISKDNSKSQVFLKMNSLQTDDTAMYYCAK	LGRGYAMDY	
RLSISKDNSKSQVFFKMNSLQADDTAIYYCAR	KRDYDYDRGYYYAMDY	
RLSISKDNSKSQVFLKMNSLQTDDTAMYYCAI	YYDGSFFAY	
RLSISKDNSKSQVFLKMNSLQTDDTARYYCAR	EGYYYFAY	
RLSISKDNSKSQVFLKMNSLQTDDTARYYCAR	IYYDGSSDYYAMDY	
RLSISKDNSKSQVFLKMNSLQTDDTAMYYCAR	13 nt.	Ps.gene/Unproductiv
RLSISKDNSKSQVFLKMNSLQTDDTAMYYCAR	21 nt.	Unproductive
RLSISKDNSKSQVFFKMNSLQADDTAIYYCAR	28 nt.	Unproductive
RLSISKDNSKSQVFLKMNSLQTDDTAMYYCAK	37 nt.	Unproductive
RLSISKDNSKSQVFLKMNSLQTDDTAMYYCAS	32 nt.	Unproductive
KATMTVDKSSSTAYMELARLTSEDSAVYYCAR	40 nt.	Unproductive
KATMTVDKSSSTAYMELARLTSEDSAVYYCAR	22 nt.	Unproductive
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCVR	RGLTYAMDY	
KATLTVDTSSSTAYMQLSSLTSEDSAVYYCAR	YYSNYFDY	
KATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR	PNWDHYYYGMDV	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTL	LYYYAMDY	
KATLTVDTSSSTAYMQLSSLTSEDSAVYYCAR	SSGYDY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTI	GAARATNAY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	GGFAY	
KATLTVDTSSSTAYMQLSSLTSEDSAVYYCAR	SPMDY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAI	EVPGGFYATDY	
KATLTVEKSSSTVYLELSRLTSDDSAVYYCAR	MDYYGSSLWFAY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAK	TTVVAFDY	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR	KRDYSTYFDH	
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAP	*TGTEFAY*	Ps.gene
*KAAWAVDTSSSTAYMQLSSLTSEDTAVYFCL**	24 nt.	Ps.gene/Unproductiv
KATLTVDKPSDTAYMQLSSLTSEDSASYYCAR	9 nt.	Unproductive
KATLTANTSSSTAYMELSSLTSEDSAVYYCAR	23 nt.	Unproductive
KATLTVDTSSSTSYMQLSSLTSEDSAVYYCAR	15 nt.	Unproductive
RFTISRDNSQSILYLQMNALRAEDSATYYCAR	YMILGAMDY	
RFTISRDNSQSILYLQMNALRAEDSATYYCAR	GYYYDGSYYAMDY	
RFTISRDNSQSILYLQMNALRAEDSATYYCAR	23 nt.	Unproductive
RFTISRDNAKNTLFLQMTSLRSEDTAMYYCAR	AKFHLYFDY	
RFIISRDNTKKTLYLQMSSLRSEDTALYYCAR	*REGVVESRLDGDV*	Ps.gene
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAD	*RGLHWFDP*	Ps.gene
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	*RNYGSSPFDY*	Ps.gene
RFIISRDNSKKTLYLQMSSLRSEDTALYYCAR	*PPMMPSY*	Ps.gene
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	43 nt.	Ps.gene/Unproductiv
RFIISRDNTKKTLYLQMSSLRSEDTALYYCAR	28 nt.	Ps.gene/Unproductiv
RFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR	35 nt.	Unproductive
RFTISRDDSKSRVYLQMNSLRAEDTGIYYCTG	30 nt.	Unproductive
KATLTADKSSSTVYMELSRLTSEDSAVYFCAR	HEDRDSSGYAMDY	

FIG. 10b

	CDR 2	FRAMEWORK 3	CDR 3
KABAT HUMAN VH1			
		STSTAYMELRSLRSEDTAVYYCAR	GEGWDHFDY
	HAQKFQG	RVTIRRHKSTSTAYMELSSLRSEDTAVYYCAR	GSRYGYDCSGYYYL
	GYAQKFQG	RVTMTRNTSISTATMELSSLRSEDTAVYYCAR	LAHFSGSPVDWFDP
KABAT HUMAN VH2			
	KHQLQPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	GGVVPAAIMDV
	KS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	MARYYDFWSGYSAYYDY
	SLKS	RLSISQDTSRNQFSLRLSSVTAADTAVYYCAR	HRNWGSPVHFDY
		ESTSTAYMELSSLRSEDTAVYYCAR	DSYGDYGGHY
KABAT HUMAN VH3			
	ISYITSSSSYTNYADSVKG	RFTISRDNAKNSLYLQMNSLRADDTAVYYCAR	DGRFGTYSPSDY
	SVKG	RFTISRDDSKSIAYLQVNSLKTEDTAVYYCTR	TIYYDSSGYPYW
	YADSVKG	RFTISRDNAKNSLFLQMSSLRAEDTAFYYCAR	GIALDAFDI
	YYADSVRD	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	53 NT. UNPROD REARR
	DSVKG	RFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR	DHSGTGGGGSGSYF
	VSAISGSGGSTYYADSVKG	RFTISRDNPKNTLYLQMNSLRSEDTAVYYCAR	KDNLWFDP
	AVISYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	DLGGRGVVVVPAPGGRSIYYYGMDV
	GAVISYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAS	LEGIGTIYYYGMDV
		AKNSLYLQMNSLRAEDTAVYYCVR	DDSSSWPKHFQH
	QYAASVKG	RFTISRDDSKNSLYLQMNSLNTEDTAVYYCVR	SGVVPYLDY
KNOWN FAMILY			
		AVYYCAR	DPRIAARPDYYYYMDV
		TAMYYCAR	GAEVVEPTARYYYGLNV

FIG. 11

FR1	CDR1	FR2
YTFT	SYGIS	WVTTGPWTRDLRWMG
GEKPGSSVKVSCKASGYTFT	DYFMN	WMRQAPGQRLEWMG
QVQLQEIGPRTGEASETLSLICAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
QVQLQESGPGLVK*SETLSLTCTVSGGSIS	SYYWS	WIrqppGKGLEWIG
GYTFT	NYCMH	WVRQDHAQGLEWMG
QVQLQESGPGLVKpSETLSLYCAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
GPRLGEASETLSLTCTVSGGSIS	SSSYYw	WIRQPPGKGLEWIG
QVQLQESGPGLVKpSETLSLTCTVSGGSIS	SYYWS	WIRQPPGKGLEWIG
LSLICAVSGSSIS	SGNW*I	WVRQPPGKGLEWIG
SETLSLTCAVYGGSFS	GYYWS	WIRQPPGKGLEWIG
QVQLVQSGAEVKKPGASVKVSCKASGYTFT	NYCMH	WVRQVLAQGLEWMG
SETLSLICAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
SRAQTGEASETLSLTCTVSGGSIS	SSSYYWG	WIRQPPGKGLEWIG
CPLTCTVSGGSVSSGS	YYWS	WIRQPPGKGLEWIG
GLVKPSETLSLTCTVSGGSIS	SYYWS	WIGSPpGKGLEWIG
SFETLSLICAVSGDSIS	SGNW*I	WVRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSVKVSCKASGGTFS	SYAIS	WVRQAPGQGLEWMG
QVQLQQWGAGLLKPSETLSLTCAVYGGSFS	GYYWS	WIRQPPGKGLEWIG
QLQLQESGPGLVKPSETLSLTCTVSGGSIS	SSSYYWG	WIRQPPGKGLEWIG
GPGLVKPSQTLSLTCTVSGGSIS	SGGYYWS	WIRQNPGKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
• sequence termonates due to internal restriction site
lower case denotes frame shift

CDR2	FR3	CDR3
WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	DTVSS
WINAGNGNTKYSQKLQG	RVTITRDTSASTAYMQLSSLRSEDTAVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLSS•	
RIYTSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSDGSTSYAQKFQA	RVTITRDTSMSTAYMELSSLRSEDTAMYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLSS•	
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS•	
YIYYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS•	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLSS•	
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSDGSTSYAQKFQA	RVTITRDTSMSTAYMELSSLRSEDTAMYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLSS•	
SIYYSGSTYYNPSLKS	RVTIPVDTSKNQFSLKLSS•	
YIYYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS
RIYTSGSTNYNPSLKS	RVTMSVDTSKNQFSLKLSS•	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLSS•	
RIIPILGIANYAQKFQG	RVTITADKSTSTAYMELSSLRSEDTAVYYCAR	DTVS
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS•	
EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS•	
YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS

FIG. 12

pSW1

HindIII site AAGCTT

```
                                        M  K  Y  L  L  P  T  A  A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
        10         20         30         40         50         60

 A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q  E  S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
        70         80         90        100        110        120

 G  P  G  L  V  A  P  S  Q  S  L  S  I  T  C  T  V  S  G  F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
       130        140        150        160        170        180

 S  L  T  G  Y  G  V  N  W  V  R  Q  P  P  G  K  G  L  E  W
TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
       190        200        210        220        230        240

 L  G  M  I  W  G  D  G  N  T  D  Y  N  S  A  L  K  S  R  L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
       250        260        270        280        290        300

 S  I  S  K  D  N  S  K  S  Q  V  F  L  K  M  N  S  L  H  T
AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
       310        320        330        340        350        360

 D  D  T  A  R  Y  Y  C  A  R  E  R  D  Y  R  L  D  Y  W  G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
       370        380        390        400        410        420

 Q  G  T  T  V  T  V  S  S                SmaI
CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGCTAAGCTCGAATTC
       430        440        450        460        470        480
```

FIG. 13

pSW2

HindIII AAGCTT

```
                                                M  K  Y  L  L  P  T  A  A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
        10        20        30        40        50        60

 A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q  E  S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
        70        80        90       100       110       120

 G  P  G  L  V  A  P  S  Q  S  L  S  I  T  C  T  V  S  G  F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
       130       140       150       160       170       180

 S  L  T  G  Y  G  V  N  W  V  R  Q  P  P  G  K  G  L  E  W
TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
       190       200       210       220       230       240

 L  G  M  I  W  G  D  G  N  T  D  Y  N  S  A  L  K  S  R  L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
       250       260       270       280       290       300

 S  I  S  K  D  N  S  K  S  Q  V  F  L  K  M  N  S  L  H  T
AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
       310       320       330       340       350       360

 D  D  T  A  R  Y  Y  C  A  R  E  R  D  Y  R  L  D  Y  W  G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
       370       380       390       400       410       420

 Q  G  T  T  V  T  V  S  S
CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
       430       440       450       460       470       480

                                M  K  Y  L  L  P  T  A  A  A  G
AAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA
       490       500       510       520       530       540

 L  L  L  L  A  A  Q  P  A  M  A  D  I  V  L  T  Q  S  P  A
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGTCCTGACTCAGTCTCCAGCC
       550       560       570       580       590       600

 S  L  S  A  S  V  G  E  T  V  T  I  T  C  R  A  S  G  N  I
TCCCTTTCTGCGTCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT
       610       620       630       640       650       660

 H  N  Y  L  A  W  Y  Q  Q  K  Q  G  K  S  P  Q  L  L  V  Y
CACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTAT
       670       680       690       700       710       720
```

FIG. 14a

```
 Y  T  T  T  L  A  D  G  V  P  S  R  F  S  G  S  G  S  G  T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA
       730        740        750        760        770        780

 Q  Y  S  L  K  I  N  S  L  Q  P  E  D  F  G  S  Y  Y  C  Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA
       790        800        810        820        830        840

 H  F  W  S  T  P  R  T  F  G  G  G  T  K  L  E  I  K  R
CATTTTTGGAGTACTCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
       850        860        870        880        890        900

TAAGAGCTCGAATTC
       910
```

FIG. 14 b

pSW1HPOLYMYC

HindIII site AAGCTT

```
                                        M  K  Y  L  L  P  T  A  A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
        10         20         30         40         50         60

 A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
        70         80         90        100        110 PstI
```

Polylinker

```
TCTAGA  GTCGAC  CTCGAG
 XbaI    SalI    XhoI
```

MYC PEPTIDE

```
  V  T  V  S  S  E  Q  K  L  I  S  E  E  D  L  N  *  *
GGTCACCGTCTCCTCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATTC
```

FIG. 15

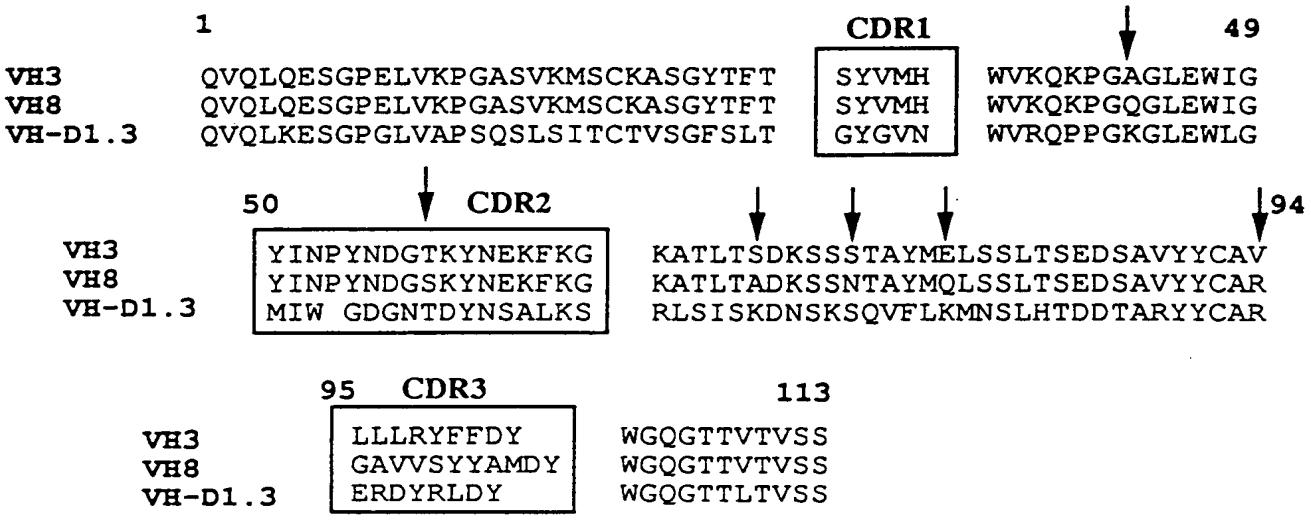


FIG. 16

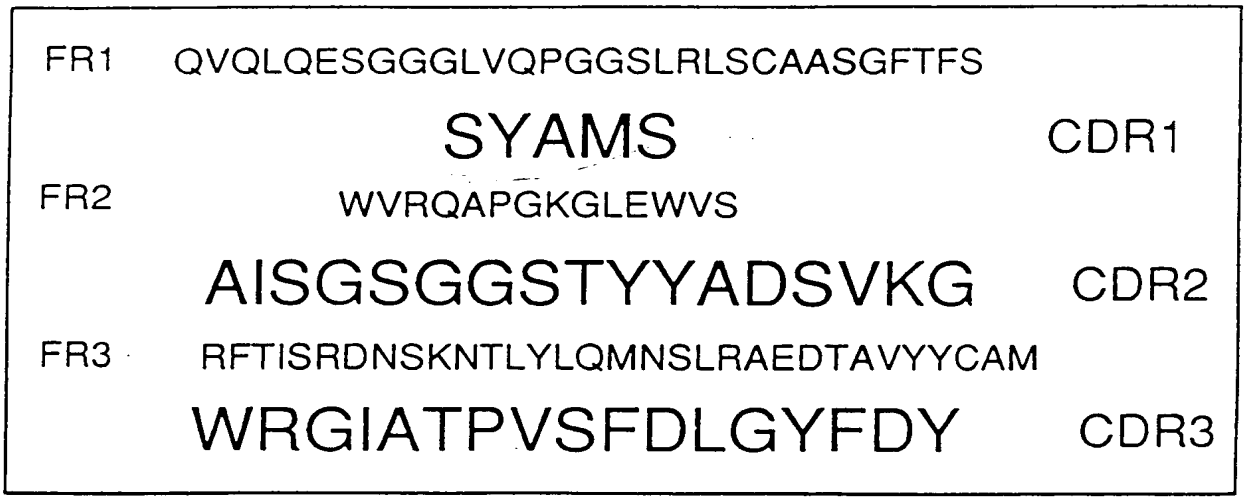


FIG. 17

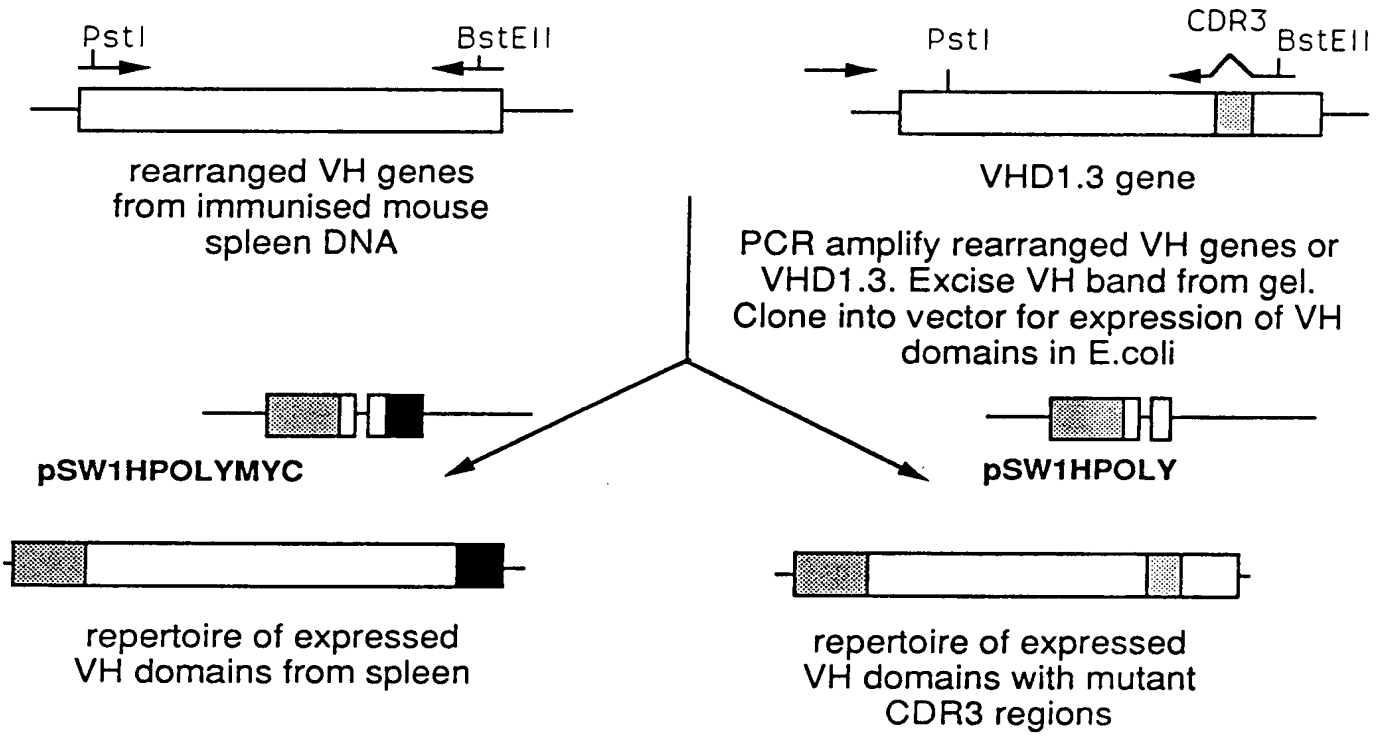


FIG. 18

pSW2HPOLY

HindIII AAGCTT

```
                                          M  K  Y  L  L  P  T  A  A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
        10        20        30        40        50        60

 A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
        70        80        90       100       110 PstI

TCTAGA GTCGAC CTCGAG
  XbaI   SalI   XhoI

  V  T  V  S  S
GGTCACCGTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
BstEII 430       440       450       460       470       480

                                    M  K  Y  L  L  P  T  A  A  A  G
AAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA
        490       500       510       520       530       540

 L  L  L  L  A  A  Q  P  A  M  A  D  I  V  L  T  Q  S  P  A
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGTCCTGACTCAGTCTCCAGCC
        550       560       570       580       590       600

 S  L  S  A  S  V  G  E  T  V  T  I  T  C  R  A  S  G  N  I
TCCCTTTCTGCGTCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT
        610       620       630       640       650       660

 H  N  Y  L  A  W  Y  Q  Q  K  Q  G  K  S  P  Q  L  L  V  Y
CACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTAT
        670       680       690       700       710       720

 Y  T  T  T  L  A  D  G  V  P  S  R  F  S  G  S  G  S  G  T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA
        730       740       750       760       770       780

 Q  Y  S  L  K  I  N  S  L  Q  P  E  D  F  G  S  Y  Y  C  Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA
        790       800       810       820       830       840

 H  F  W  S  T  P  R  T  F  G  G  G  T  K  L  E  I  K  R
CATTTTTGGAGTACTCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
        850       860       870       880       890       900

TAAGAGCTCGAATTC
        910
```

FIG. 19

```
                                                          M  K  Y  L  L  P  T
AAGCTTGCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG
        10         20         30         40         50         60

 A  A  A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q
GCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
        70         80         90        100        110        120

 E  S  G  P  G  L  V  A  P  S  Q  S  L  S  I  T  C  T  V  S
GAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCA
       130        140        150        160        170        180

 G  F  S  L  T  G  Y  G  V  N  W  V  R  Q  P  P  G  K  G  L
GGGTTCTCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTG
       190        200        210        220        230        240

 E  W  L  G  M  I  W  G  D  G  N  T  D  Y  N  S  A  L  K  S
GAGTGGCTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCC
       250        260        270        280        290        300

 R  L  S  I  S  K  D  N  S  K  S  Q  V  F  L  K  M  N  S  L
AGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTG
       310        320        330        340        350        360

 H  T  D  D  T  A  R  Y  Y  C  A  R  E  R  D  Y  R  L  D  Y
CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTAC
       370        380        390        400        410        420

 W  G  Q  G  T  T  V  T  V  S  S  G  G  G  A  P  A  A  A  P
TGGGGCCAAGGCACCACGGTCACCGTCTCCTCAGGTGGTGGTGCTCCAGCAGCTGCACCT
       430        440        450        460        470        480

 A  G  G  G  Q  V  Q  L  K  E  S  G  P  G  L  V  A  P  S  Q
GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAG
       490        500        510        520        530        540

 S  L  S  I  T  C  T  V  S  G  F  S  L  T  G  Y  G  V  N  W
AGCCTGTCCATCACATGCACCGTCTCAGGGTTCTCATTAACCGGCTATGGTGTAAACTGG
       550        560        570        580        590        600

 V  R  Q  P  P  G  K  G  L  E  W  L  G  M  I  W  G  D  G  N
GTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAAC
       610        620        630        640        650        660

 T  D  Y  N  S  A  L  K  S  R  L  S  I  S  K  D  N  S  K  S
ACAGACTATAATTCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGC
       670        680        690        700        710        720

 Q  V  F  L  K  M  N  S  L  H  T  D  D  T  A  R  Y  Y  C  A
CAAGTTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC
       730        740        750        760        770        780

 R  E  R  D  Y  R  L  D  Y  W  G  Q  G  T  T  V  T  V  S  S
AGAGAGAGAGATTATAGGCTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTCCTCA
       790        800        810        820        830        840
 *  *
TAATAAGAGCTC
       850
```

FIG. 20

```
                                                        M  K  Y  L  L  P  T  A  A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
         10         20         30         40         50         60

 A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q  E  S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
         70         80         90        100        110        120

 G  P  G  L  V  A  P  S  Q  S  L  S  I  T  C  T  V  S  G  F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
        130        140        150        160        170        180

 S  L  T  G  Y  G  V  N  W  V  R  Q  P  P  G  K  G  L  E  W
TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
        190        200        210        220        230        240

 L  G  M  I  W  G  D  G  N  T  D  Y  N  S  A  L  K  S  R  L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
        250        260        270        280        290        300

 S  I  S  K  D  N  S  K  S  Q  V  F  L  K  M  N  S  L  H  T
AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
        310        320        330        340        350        360

 D  D  T  A  R  Y  Y  C  A  R  E  R  D  Y  R  L  D  Y  W  G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
        370        380        390        400        410        420

 Q  G  T  T  V  T  V  S  S  R  T  P  E  M  P  V  L  E  N  R
CAAGGCACCACGGTCACCGTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAAAACCGG
        430        440        450        460        470        480

 A  A  Q  G  D  I  T  A  P  G  G  A  R  R  L  T  G  D  Q  T
GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTTAACGGGTGATCAGACT
        490        500        510        520        530        540

 A  A  L  R  D  S  L  S  D  K  P  A  K  N  I  I  L  L  I  G
GCCGCTCTGCGTGATTCTCTTAGCGATAAACCTGCAAAAAATATTATTTTGCTGATTGGC
        550        560        570        580        590        600

 D  G  M  G  D  S  E  I  T  A  A  R  N  Y  A  E  G  A  G  G
GATGGGATGGGGGACTCGGAAATTACTGCCGCACGTAATTATGCCGAAGGTGCGGGCGGC
        610        620        630        640        650        660

 F  F  K  G  I  D  A  L  P  L  T  G  Q  Y  T  H  Y  A  L  N
TTTTTTAAAGGTATAGATGCCTTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
        670        680        690        700        710        720

 K  K  T  G  K  P  D  Y  V  T  D  S  A  A  S  A  T  A  W  S
AAAAAAACCGGCAAACCGGACTACGTCACCGACTCGGCTGCATCAGCAACCGCCTGGTCA
        730        740        750        760        770        780
```

FIG. 21a

```
 T  G  V  K  T  Y  N  G  A  L  G  V  D  I  H  E  K  D  H  P
ACCGGTGTCAAAACCTATAACGGCGCGCTGGGCGTCGATATTCACGAAAAAGATCACCCA
      790        800        810        820        830        840

 T  I  L  E  M  A  K  A  A  G  L  A  T  G  N  V  S  T  A  E
ACGATTCTGGAAATGGCAAAAGCCGCAGGTCTGGCGACCGGTAACGTTTCTACCGCAGAG
      850        860        870        880        890        900

 L  Q  D  A  T  P  A  A  L  V  A  H  V  T  S  R  K  C  Y  G
TTGCAGGATGCCACGCCCGCTGCGCTGGTGGCACATGTGACCTCGCGCAAATGCTACGGT
      910        920        930        940        950        960

 P  S  A  T  S  E  K  C  P  G  N  A  L  E  K  G  G  K  G  S
CCGAGCGCGACCAGTGAAAAATGTCCGGGTAACGCTCTGGAAAAAGGCGGAAAAGGATCG
      970        980        990       1000       1010       1020

 I  T  E  Q  L  L  N  A  R  A  D  V  T  L  G  G  G  A  K  T
ATTACCGAACAGCTGCTTAACGCTCGTGCCGACGTTACGCTTGGCGGCGGCGCAAAAACC
     1030       1040       1050       1060       1070       1080

 F  A  E  T  A  T  A  G  E  W  Q  G  K  T  L  R  E  Q  A  Q
TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGGAAAAACGCTGCGTGAACAGGCACAG
     1090       1100       1110       1120       1130       1140

 A  R  G  Y  Q  L  V  S  D  A  A  S  L  N  S  V  T  E  A  N
GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTCACTGAATTCGGTGACGGAAGCGAAT
     1150       1160       1170       1180       1190       1200

 Q  Q  K  P  L  L  G  L  F  A  D  G  N  M  P  V  R  W  L  G
CAGCAAAAACCCCTGCTTGGCCTGTTTGCTGACGGCAATATGCCAGTGCGCTGGCTAGGA
     1210       1220       1230       1240       1250       1260

 P  K  A  T  Y  H  G  N  I  D  K  P  A  V  T  C  T  P  N  P
CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
     1270       1280       1290       1300       1310       1320

 Q  R  N  D  S  V  P  T  L  A  Q  M  T  D  K  A  I  E  L  L
CAACGTAATGACAGTGTACCAACCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
     1330       1340       1350       1360       1370       1380

 S  K  N  E  K  G  F  F  L  Q  V  E  G  A  S  I  D  K  Q  D
AGTAAAAATGAGAAAGGCTTTTTCCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGAT
     1390       1400       1410       1420       1430       1440

 H  A  A  N  P  C  G  Q  I  G  E  T  V  D  L  D  E  A  V  Q
CATGCTGCGAATCCTTGTGGGCAAATTGGCGAGACGGTCGATCTCGATGAAGCCGTACAA
     1450       1460       1470       1480       1490       1500

 R  A  L  E  F  A  K  K  E  G  N  T  L  V  I  V  T  A  D  H
CGGGCGCTGGAATTCGCTAAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
     1510       1520       1530       1540       1550       1560
```

FIG. 21b

```
 A  H  A  S  Q  I  V  A  P  D  T  K  A  P  G  L  T  Q  A  L
GCCCACGCCAGCCAGATTGTTGCGCCGGATACCAAAGCTCCGGGCCTCACCCAGGCGCTA
      1570       1580       1590       1600       1610       1620

 N  T  K  D  G  A  V  M  V  M  S  Y  G  N  S  E  E  D  S  Q
AATACCAAAGATGGCGCAGTGATGGTGATGAGTTACGGGAACTCCGAAGAGGATTCACAA
      1630       1640       1650       1660       1670       1680

 E  H  T  G  S  Q  L  R  I  A  A  Y  G  P  H  A  A  N  V  V
GAACATACCGGCAGTCAGTTGCGTATTGCGGCGTATGGCCCGCATGCCGCCAATGTTGTT
      1690       1700       1710       1720       1730       1740

 G  L  T  D  Q  T  D  L  F  Y  T  M  K  A  A  L  G  L  K  *
GGACTGACCGACCAGACCGATCTCTTCTACACCATGAAAGCCGCTCTGGGGCTGAAATAA
      1750       1760       1770       1780       1790       1800

AACCGCGCCCGGGAGTGAATTTTCGCTGCCGGGTGGTTTTTTTGCTGTTAGC
      1810       1820       1830       1840       1850
```

FIG. 21c

```
                                                    M  K  Y  L  L  P  T  A  A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
        10         20         30         40         50         60

 A  G  L  L  L  L  A  A  Q  P  A  M  A  Q  V  Q  L  Q  E  S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
        70         80         90        100        110        120

 G  P  G  L  V  A  P  S  Q  S  L  S  I  T  C  T  V  S  G  F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
       130        140        150        160        170        180

 S  L  T  G  Y  G  V  N  W  V  R  Q  P  P  G  K  G  L  E  W
TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
       190        200        210        220        230        240

 L  G  M  I  W  G  D  G  N  T  D  Y  N  S  A  L  K  S  R  L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
       250        260        270        280        290        300

 S  I  S  K  D  N  S  K  S  Q  V  F  L  K  M  N  S  L  H  T
AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
       310        320        330        340        350        360

 D  D  T  A  R  Y  Y  C  A  R  E  R  D  Y  R  L  D  Y  W  G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
       370        380        390        400        410        420

 Q  G  T  T  V  T  V  S  S  *  *
CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGAGCTTGCATGCAAA
       430        440        450        460        470        480

                              M  K  Y  L  L  P  T  A  A  A  G  L
TTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
       490        500        510        520        530        540

 L  L  L  A  A  Q  P  A  M  A  D  I  E  L  V  D  L  E  I  K
TTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAAA
       550        560        570        580        590        600

 R  E  Q  K  L  I  S  E  E  D  L  N  *  *
CGGGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
       610        620        630        640        650        660

GATCCAGCTCGAATTC
       670
```

FIG. 22

```
                                                A
 Q  V  Q  L  Q  E  S  G  P  G  L  V  Q  P  S  Q  S  L  S  I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC

        10         20         30         40         50         60

                                    G              N              P
 T  C  T  V  S  G  F  S  L  T  S  Y  G  V  H  W  V  R  Q  S
ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCAGTCT
                                                               C
        70         80         90        100        110        120

 P  G  K  G  L  E  W  L  G  M  I  W  G  D  G  N  T  D  Y  N
CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAACACAGACTATAAT
       130        140        150        160        170        180

 S  A  L  K  S  R  L  S  I  S  K  D  N  S  K  S  Q  V  F  L
TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTA
       190        200        210        220        230        240

 K  M  N  S  L  H  T  D  D  T  A  R  Y  Y  C  A  R  E  R  D
AAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGAT
       250        260        270        280        290        300

 Y  R  L  D  Y  W  G  Q  G  T  T  V  T  V  S  S
TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
       310        320        330        340
```

FIG. 23